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Suggestions

This page gives you Search Results detail for the Application 10772774 and Search Result 20070125_125134_us-10-772-774-287.rup.

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OM protein - protein search, using sw model

```
Run on:      January 28, 2007, 06:03:56 ; Search time 348 Seconds
              (without alignments)
              21.566 Million cell updates/sec
```

```
Title:      US-10-772-774-287
Perfect score: 36
Sequence:   1 GAGXPYN 7
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 500 summaries
```

```
Database :      UniProt_8.4:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	100.0	123	2	Q9YA10_AERPE	Q9ya10 aeropyrum p
2	36	100.0	382	2	P91703_DROSU	P91703 drosophila
3	36	100.0	542	2	Q5FM11_LACAC	Q5fm11 lactobacill

SCORE Search Results Details for Application 10772774 and Search Result 20070125_125138 10-772-774-287.ra1.

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OM protein - protein search, using sw model

Run on: January 28, 2007, 06:13:51 ; Search time 51 Seconds
(without alignments)
12.014 Million cell updates/sec

Title: US-10-772-774-287
Perfect score: 36
Sequence: 1 GAGXPYN 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query
No.	Score	Match Length DB ID Description

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OM protein - protein search, using sw model

Run on: January 28, 2007, 06:14:21 ; Search time 189 Seconds
(without alignments)
17.156 Million cell updates/sec

Title: US-10-772-774-287
Perfect score: 36
Sequence: 1 GAGXPYN 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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OM protein - protein search, using sw model

Run on: January 28, 2007, 06:15:12 ; Search time 52 Seconds
(without alignments)
16.499 Million cell updates/sec

Title: US-10-772-774-287
Perfect score: 36
Sequence: 1 GAGXPYN 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 507816 seqs, 122560497 residues

Total number of hits satisfying chosen parameters: 507816

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published Applications_AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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